

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/898,556A

CRF Processing Date: 3/7/2002

Edited by: [Signature]

Verified by: [Signature] (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95



OIPE

RAW SEQUENCE LISTING

DATE: 03/07/2002

PATENT APPLICATION: US/09/898,556A

TIME: 19:05:08

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03072002\I898556A.raw

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3 <110> APPLICANT: C. Frank Bennett
4   Susan M. Freier
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
8 <130> FILE REFERENCE: RTS-0248
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/898,556A
C--> 10 <141> CURRENT FILING DATE: 2001-07-03
10 <160> NUMBER OF SEQ ID NOS: 89
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 20
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: Antisense Oligonucleotide
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25 <210> SEQ ID NO: 2
26 <211> LENGTH: 20
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Antisense Oligonucleotide
33 <400> SEQUENCE: 2
34 atgcattctg cccccaagga                                20
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 2772
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <220> FEATURE:
44 <221> NAME/KEY: CDS
45 <222> LOCATION: (3)...(2096)
47 <400> SEQUENCE: 3
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49   Gly Ala Leu Ser Trp Leu Gly Pro Gly Lys Ala Ser Leu Leu Arg
50     1         5         10         15
52 tct ttc cca cac ctc tgc tcc ttg tta cct gac ttt cgg ctt cag gat    95
53 Ser Phe Pro His Leu Cys Ser Leu Leu Pro Asp Phe Arg Leu Gln Asp
54           20           25           30
56 ccg cgg cgt gca ccc gcg ttc cat ctg tct tct gag act ttg ccc ttc    143
57 Pro Arg Arg Ala Pro Ala Phe His Leu Ser Ser Glu Thr Leu Pro Phe
58       35       40       45
60 tcc agg aag agc act cag gag acc agg aaa atg gct aca ggg ctc ctg    191
61 Ser Arg Lys Ser Thr Gln Glu Thr Arg Lys Met Ala Thr Gly Leu Leu
62       50       55       60

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64 aga gcc aaa aaa gag gcg ttc gtg gca ttc agg gat gtg gct gtg tac 239
65 Arg Ala Lys Lys Glu Ala Phe Val Ala Phe Arg Asp Val Ala Val Tyr
66      65      70      75
68 ttc acc cag gag gag tgg agg ttg ttg agc cct gct cag agg acc ctg 287
69 Phe Thr Gln Glu Glu Trp Arg Leu Leu Ser Pro Ala Gln Arg Thr Leu
70 80      85      90      95
72 cac agg gag gtg atg ctg gag act tat aac cat ctg gtc tca ctg gaa 335
73 His Arg Glu Val Met Leu Glu Thr Tyr Asn His Leu Val Ser Leu Glu
74      100      105      110
76 att cca tct tct aaa cca aaa ctc att gct cag ctg gag cga ggg gaa 383
77 Ile Pro Ser Ser Lys Pro Lys Leu Ile Ala Gln Leu Glu Arg Gly Glu
78      115      120      125
80 gcg ccc tgg aga gag gag aga aaa tgt cca ctg gac ctc tgt cca gaa 431
81 Ala Pro Trp Arg Glu Glu Arg Lys Cys Pro Leu Asp Leu Cys Pro Glu
82      130      135      140
84 tcg aag cca gaa att caa ctt agt ccc tcc tgc cct ctg att ttc tcc 479
85 Ser Lys Pro Glu Ile Gln Leu Ser Pro Ser Cys Pro Leu Ile Phe Ser
86      145      150      155
88 agt cag caa gct ctc agc caa cat gtg tgg ctg agt cat ctc tct cag 527
89 Ser Gln Gln Ala Leu Ser Gln His Val Trp Leu Ser His Leu Ser Gln
90 160      165      170      175
92 ctg ttt tca agt tta tgg gca gga aat cct ctc cac ctg gga aaa cac 575
93 Leu Phe Ser Ser Leu Trp Ala Gly Asn Pro Leu His Leu Gly Lys His
94      180      185      190
96 tat cca gaa gat cag aaa caa cag cag gat cca ttc tgc ttt agt ggc 623
97 Tyr Pro Glu Asp Gln Lys Gln Gln Asp Pro Phe Cys Phe Ser Gly
98      195      200      205
100 aaa gca gaa tgg att caa gag gga gaa gac tcc aga ctc ctg ttt ggg 671
101 Lys Ala Glu Trp Ile Gln Glu Gly Glu Asp Ser Arg Leu Leu Phe Gly
102      210      215      220
104 aga gta agc aaa aat ggc act tca aag gca ctt tcc agc cca cct gaa 719
105 Arg Val Ser Lys Asn Gly Thr Ser Lys Ala Leu Ser Ser Pro Pro Glu
106      225      230      235
108 gaa caa cag cca gca cag tcc aag gaa gac aac aca gtg gtg gat ata 767
109 Glu Gln Gln Pro Ala Gln Ser Lys Glu Asp Asn Thr Val Val Asp Ile
110 240      245      250      255
112 ggg tcc agc cct gaa cgg agg gca gat cta gag gaa aca gac aaa gta 815
113 Gly Ser Ser Pro Glu Arg Arg Ala Asp Leu Glu Glu Thr Asp Lys Val
114      260      265      270
116 ttg cat ggt tta gaa gtc tca gga ttt gga gaa atc aaa tat gaa gag 863
117 Leu His Gly Leu Glu Val Ser Gly Phe Gly Glu Ile Lys Tyr Glu Glu
118      275      280      285
120 ttt ggg cca ggc ttt atc aag gag tca aac ctc ctt agc ctc cag aag 911
121 Phe Gly Pro Gly Phe Ile Lys Glu Ser Asn Leu Leu Ser Leu Gln Lys
122      290      295      300
124 aca caa act ggg gag aca cct tac atg tac act gag tgg gga gac agc 959
125 Thr Gln Thr Gly Glu Thr Pro Tyr Met Tyr Thr Glu Trp Gly Asp Ser
126      305      310      315
128 ttt ggc agt atg tca gtc ctc atc aaa aac cca agg aca cac tct ggg 1007

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130	320					325					330					335	
132	gga	aag	cct	tat	gtg	tgc	agg	gaa	tgt	ggg	cga	ggc	ttt	acg	tgg	aag	1055
133	Gly	Lys	Pro	Tyr	Val	Cys	Arg	Glu	Cys	Gly	Arg	Gly	Phe	Thr	Trp	Lys	
134					340					345						350	
136	tca	aac	ctg	atc	aca	cat	cag	agg	aca	cac	tca	ggg	gag	aaa	cct	tat	1103
137	Ser	Asn	Leu	Ile	Thr	His	Gln	Arg	Thr	His	Ser	Gly	Glu	Lys	Pro	Tyr	
138					355					360						365	
140	gtg	tgc	aag	gat	tgt	gga	cga	ggc	ttt	act	tgg	aag	tcg	aac	ctc	ttt	1151
141	Val	Cys	Lys	Asp	Cys	Gly	Arg	Gly	Phe	Thr	Trp	Lys	Ser	Asn	Leu	Phe	
142			370					375					380				
144	aca	cat	cag	cgg	aca	cac	tca	ggg	ctc	aag	cct	tat	gtg	tgc	aag	gaa	1199
145	Thr	His	Gln	Arg	Thr	His	Ser	Gly	Leu	Lys	Pro	Tyr	Val	Cys	Lys	Glu	
146			385					390					395				
148	tgt	ggg	cag	agc	ttt	agc	ctg	aag	tca	aac	ctc	att	acc	cac	cag	agg	1247
149	Cys	Gly	Gln	Ser	Phe	Ser	Leu	Lys	Ser	Asn	Leu	Ile	Thr	His	Gln	Arg	
150	400					405					410					415	
152	gcg	cac	act	ggg	gag	aag	cct	tat	gtt	tgc	agg	gaa	tgt	ggg	cgt	ggc	1295
153	Ala	His	Thr	Gly	Glu	Lys	Pro	Tyr	Val	Cys	Arg	Glu	Cys	Gly	Arg	Gly	
154					420					425						430	
156	ttt	cgc	cag	cat	tca	cac	ctg	gtc	aga	cac	aag	agg	aca	cat	tca	gga	1343
157	Phe	Arg	Gln	His	Ser	His	Leu	Val	Arg	His	Lys	Arg	Thr	His	Ser	Gly	
158				435					440					445			
160	gag	aag	cct	tac	att	tgc	agg	gag	tgt	gag	caa	ggc	ttt	agc	cag	aag	1391
161	Glu	Lys	Pro	Tyr	Ile	Cys	Arg	Glu	Cys	Glu	Gln	Gly	Phe	Ser	Gln	Lys	
162			450					455					460				
164	tca	cac	ctc	atc	aga	cac	tta	agg	aca	cac	aca	gga	gag	aag	cct	tat	1439
165	Ser	His	Leu	Ile	Arg	His	Leu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	
166			465				470					475					
168	gta	tgc	aca	gaa	tgt	ggg	cgt	cac	ttt	agc	tgg	aaa	tca	aac	ctc	aaa	1487
169	Val	Cys	Thr	Glu	Cys	Gly	Arg	His	Phe	Ser	Trp	Lys	Ser	Asn	Leu	Lys	
170	480					485					490					495	
172	aca	cac	cag	agg	aca	cac	tca	ggg	gtt	aaa	cct	tat	gtc	tgc	ctg	gag	1535
173	Thr	His	Gln	Arg	Thr	His	Ser	Gly	Val	Lys	Pro	Tyr	Val	Cys	Leu	Glu	
174					500					505						510	
176	tgc	ggg	cag	tgc	ttt	agc	ctg	aag	tca	aac	ctt	aac	aaa	cac	cag	agg	1583
177	Cys	Gly	Gln	Cys	Phe	Ser	Leu	Lys	Ser	Asn	Leu	Asn	Lys	His	Gln	Arg	
178				515					520					525			
180	tca	cac	acg	ggg	gag	aag	cca	ttt	gta	tgt	acg	gag	tgt	ggg	cga	ggc	1631
181	Ser	His	Thr	Gly	Glu	Lys	Pro	Phe	Val	Cys	Thr	Glu	Cys	Gly	Arg	Gly	
182			530					535					540				
184	ttt	acc	cgg	aaa	tca	acc	ctg	atc	acg	cac	cag	agg	aca	cac	tca	ggg	1679
185	Phe	Thr	Arg	Lys	Ser	Thr	Leu	Ile	Thr	His	Gln	Arg	Thr	His	Ser	Gly	
186			545				550					555					
188	gag	aag	cca	ttt	gta	tgt	gct	gag	tgt	gga	cga	ggc	ttt	aat	gat	aag	1727
189	Glu	Lys	Pro	Phe	Val	Cys	Ala	Glu	Cys	Gly	Arg	Gly	Phe	Asn	Asp	Lys	
190	560					565					570					575	
192	tcc	acc	ctc	att	tca	cac	cag	agg	aca	cat	tca	ggg	gaa	aag	cct	ttt	1775
193	Ser	Thr	Leu	Ile	Ser	His	Gln	Arg	Thr	His	Ser	Gly	Glu	Lys	Pro	Phe	

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196 atg tgc agg gag tgt ggc aga agg ttt cgg cag aag cct aac ctg ttt 1823
197 Met Cys Arg Glu Cys Gly Arg Arg Phe Arg Gln Lys Pro Asn Leu Phe
198          595          600          605
200 agg cac aag agg gca cac tca ggt gcc ttt gtg tgc agg gag tgt ggg 1871
201 Arg His Lys Arg Ala His Ser Gly Ala Phe Val Cys Arg Glu Cys Gly
202          610          615          620
204 caa ggc ttt tgt gct aag tta act ctc att aaa cac cag aga gca cac 1919
205 Gln Gly Phe Cys Ala Lys Leu Thr Leu Ile Lys His Gln Arg Ala His
206          625          630          635
208 gca ggg ggg aag cct cat gtg tgc agg gag tgt ggg caa ggc ttt agc 1967
209 Ala Gly Gly Lys Pro His Val Cys Arg Glu Cys Gly Gln Gly Phe Ser
210 640          645          650          655
212 cgg cag tca cac ctc att aga cac cag agg aca cat tca gga gag aag 2015
213 Arg Gln Ser His Leu Ile Arg His Gln Arg Thr His Ser Gly Glu Lys
214          660          665          670
216 cct tat att tgc aga aag tgt gga cgg ggc ttt agt cgg aag tcc aac 2063
217 Pro Tyr Ile Cys Arg Lys Cys Gly Arg Gly Phe Ser Arg Lys Ser Asn
218          675          680          685
220 ctt atc aga cat cag agg aca cac tca gga tag aaactttatg tgtataggga 2116
221 Leu Ile Arg His Gln Arg Thr His Ser Gly
222          690          695
224 atgtggtaca gcccttagcc aggagtcata cttcatcaga caccagagga cacacacagt 2176
226 gctgtggcctt tttcagccat tgctagatac caaagtggag acattctgtg tgtgattatg 2236
228 catgagactg tactggtaag acttgtatct ccatccacct gaaggagaat tgctggctca 2296
230 ttttcaggag ccttgccctt cctcactgtg gatggtgggt tgtggaaacc cggtcaggta 2356
232 atgatatggg caggaggcag tcaaatgccc aggcagatag ggggtgggtac ctggtgaaac 2416
234 ccaaccttaa agctgaagac agtcccggct aaatcctcat actgaattga gaacctgtct 2476
236 tcccatttgg tgtgctttcc tccgattgat cccaaccctt cacctatatt acgtatacct 2536
238 gccctttcct aattggtttt tacactgetg tgcccacctt ttgagtgggt cctttgcata 2596
240 cttacaaatc agtcaacgtg tattccccta ttctgagccc ataaaagacc cagactcagc 2656
242 tgcagtgagg agagaaatca cctgctgtg gaggttggg accactccct gcacccctc 2716
244 tccactgaga gctgttcttt tgctcaataa aattcttttc taccatcct caccct 2772
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250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR Primer
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264 <220> FEATURE:
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267 <400> SEQUENCE: 5
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Input Set : A:\PTO.AMC.txt

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273 <212> TYPE: DNA
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276 <220> FEATURE:
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284 <211> LENGTH: 19
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: PCR Primer
291 <400> SEQUENCE: 7
292 gaaggtgaag gtcggagtc                19
295 <210> SEQ ID NO: 8
296 <211> LENGTH: 20
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: PCR Primer
303 <400> SEQUENCE: 8
304 gaagatggtg atgggatttc                20
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308 <211> LENGTH: 20
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: PCR Probe
315 <400> SEQUENCE: 9
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320 <211> LENGTH: 11173
321 <212> TYPE: DNA
322 <213> ORGANISM: Homo sapiens
324 <220> FEATURE:
326 <400> SEQUENCE: 10
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329 ttcaatatat ttctgtccc ttttactctt tctctcatt ctaggactcc caatttacct    120
331 gtatatgga ctgctgaaa tgtgtttctg aagattcata ttgtctcata agcttcgtt    180
333 catttttctt cagtcctttt tctctttttt gaggggtggg tggatatatg taatttctat    240
335 tcttttatat tcaaattcac taatctttct tctttttctg tttgctatta aacctgtcta    300
337 gtgaattttt aaatttcagt tgttttttct tttccccctc cctcctctc cctcctctc    360
339 cctccccctc cctccccctc cctccccctc cctccccctc cctccccctc ctcttgtttc    420
341 tgtgggtttt aggagtgtc tcaggcaaga aagccacaaa caaaattatt acccctttct    480
343 gttgcaattt tttgagcata aactcttccc catcttctgg ctggttatgt atattttcca    540
345 gtgcctttga gtagttatit gttatatit atccagtctt attattttct gctgcagggt    600
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VERIFICATION SUMMARY

DATE: 03/07/2002

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TIME: 19:05:09

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03072002\I898556A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date